<110> U.S. Army Medical Research & Material Command

<120> RECOMBINANT VACCINE AGAINST BOTULINUM
  NEUROTOXIN

<130> A33626-A 067252.0107

<150> PCT/US00/12890
<151> 2000-05-12

<150> 09/611,419
<151> 2000-07-06

<150> 60/133,865
<151> 1999-05-12

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<151> 1993-09-21

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            Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn
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atc atc aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg   99
Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu
     15   20   25

atc gac ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt   147
Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val

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aac ttc gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa    195
Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu
                50                  55                  60

tct tcc aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct    243
Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser
            65                  70                  75

atg tac gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac    291
Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr
        80                  85                  90

ttc aac tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg    339
Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met
        95                  100                 105

gaa aac aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc    387
Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile
110                 115                 120                 125

tgg act ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa    435
Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys
                130                 135                 140

tac tct cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc    483
Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe
                145                 150                 155

gtt acc atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac    531
Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn
            160                 165                 170

ggc cgt ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac    579
Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His
        175                 180                 185

gct tct aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac    627
Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His
190                 195                 200                 205

cgc tac atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac    675
Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn
                210                 215                 220

gaa aaa gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc    723
Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile
                225                 230                 235

ctg aaa gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac    771
Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr
        240                 245                 250

atg ctg aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta    819
Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val
        255                 260                 265

ggt atc cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg    867
Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met
270                 275                 280                 285
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act acc aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc     915
Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe
            290                 295                 300

atc atc aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac     963
Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn
            305                 310                 315

aat gat cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt    1011
Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg
            320                 325                 330

ctg gct acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct    1059
Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala
            335                 340                 345

ctg gaa atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa    1107
Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys
350                 355                 360                 365

tcc aag aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag    1155
Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln
            370                 375                 380

gac aac aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac    1203
Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn
            385                 390                 395

aat atc gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa    1251
Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu
            400                 405                 410

cgt tcc tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat    1299
Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp
            415                 420                 425

gac ggt tgg ggt gaa cgt ccg ctg taa gaattc                        1332
Asp Gly Trp Gly Glu Arg Pro Leu  *
430                 435
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<210> 2
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<212> PRT
<213> Synthetic Construct

<220>

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Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
            20                  25                  30
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
            35                  40                  45
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
      50                  55                  60
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
65                  70                  75                  80
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Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
                85   90   95
Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
            100   105   110
Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
            115   120   125
Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
    130   135   140
Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
145   150   155   160
Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
                165   170   175
Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
            180   185   190
Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
            195   200   205
Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
    210   215   220
Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
225   230   235   240
Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
                245   250   255
Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
            260   265   270
Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
            275   280   285
Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
            290   295   300
Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
305   310   315   320
Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
                325   330   335
Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
            340   345   350
Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn
            355   360   365
Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn
            370   375   380
Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala
385   390   395   400
Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser
                405   410   415
Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp
            420   425   430
Gly Glu Arg Pro Leu
            435

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<222> (13)...(1314)
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acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac ctg 99
Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
    15   20   25

tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc gat 147
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
30   35   40   45

ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc aaa 195
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
                50   55   60

atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac gaa 243
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
                65   70   75

aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac tcc 291
Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
        80   85   90

atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac aat 339
Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
    95   100   105

tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act ctg 387
Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
110   115   120   125

cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct cag 435
Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
                130   135   140

atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc atc 483
Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
            145   150   155

acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt ctg 531
Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
        160   165   170

atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct aat 579
Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
    175   180   185

aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac atc 627
Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
190   195   200   205

tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa gaa 675
Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
                210   215   220

atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa gac 723
Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
            225   230   235

ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg aat 771

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          Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
              240                 245                 250

ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc cgc        819
Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
    255                 260                 265

ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg act acc aac        867
Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
270                 275                 280                 285

atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc atc atc aag        915
Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
                290                 295                 300

aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac aat gat cgt        963
Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
            305                 310                 315

gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt ctg gct acc       1011
Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
            320                 325                 330

aat gct tct cag gct ggt gta gaa aag atc ttg tct gct ctg gaa atc       1059
Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
    335                 340                 345

ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa tcc aag aac       1107
Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn
350                 355                 360                 365

gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag gac aac aat       1155
Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn
                370                 375                 380

ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac aat atc gct       1203
Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala
            385                 390                 395

aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa cgt tcc tct       1251
Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser
    400                 405                 410

cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat gac ggt tgg       1299
Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp
    415                 420                 425

ggt gaa cgt ccg ctg taagaattc                                         1323
Gly Glu Arg Pro Leu
430
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<211> 434
<212> PRT
<213> Synthetic Construct

<220>

<400> 4

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Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr
            20              25              30
Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp
        35              40              45
Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val
    50              55              60
Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser
65              70              75              80
Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu
            85              90              95
Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp
            100             105             110
Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr
            115             120             125
Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn
    130             135             140
Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn
145             150             155             160
Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln
            165             170             175
Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met
            180             185             190
Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys
            195             200             205
Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp
    210             215             220
Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly
225             230             235             240
Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp
            245             250             255
Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met
            260             265             270
Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu
    275             280             285
Asn Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala
    290             295             300
Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile
305             310             315             320
Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser
            325             330             335
Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val
            340             345             350
Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly
    355             360             365
Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp
    370             375             380
Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val
385             390             395             400
Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu
            405             410             415
Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg
            420             425             430
Pro Leu
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            1               5                   10

aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac   99
Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp
     15                  20                  25

ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc  147
Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe
 30                  35                  40                  45

gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc  195
Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser
                 50                  55                  60

aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac  243
Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr
                     65                  70                  75

gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac  291
Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn
             80                  85                  90

tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac  339
Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn
     95                  100                 105

aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act  387
Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr
110                 115                 120                 125

ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct  435
Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser
                 130                 135                 140

cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc  483
Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr
             145                 150                 155

atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt  531
Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg
         160                 165                 170

ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct  579
Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser
     175                 180                 185

aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac  627
Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr
190                 195                 200                 205
```

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atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa   675
Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys
            210             215             220

gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa   723
Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys
            225             230             235

gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg   771
Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu
            240             245             250

aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc   819
Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile
            255             260             265

cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg act acc   867
Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr
270             275             280             285

aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc atc atc   915
Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile
            290             295             300

aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac aat gat   963
Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp
            305             310             315

cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt ctg gct  1011
Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala
            320             325             330

acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct ctg gaa  1059
Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu
            335             340             345

atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa tcc aag  1107
Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys
350             355             360             365

aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag gac aac  1155
Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn
            370             375             380

aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac aat atc  1203
Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile
            385             390             395

gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa cgt tcc  1251
Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser
            400             405             410

tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat gac ggt  1299
Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly
            415             420             425

tgg ggt gaa cgt ccg ctg taagaattc                                 1326
Trp Gly Glu Arg Pro Leu
430             435
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<210> 6
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<212> PRT
<213> Synthetic Construct

<220>

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Met Ala Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser
 1               5                  10                  15
Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg
            20                  25                  30
Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile
            35                  40                  45
Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Lys Ile Glu
    50                  55                  60
Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe
65                  70                  75                  80
Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser
                85                  90                  95
Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly
            100                 105                 110
Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp
            115                 120                 125
Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile
    130                 135                 140
Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn
145                 150                 155                 160
Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp
                165                 170                 175
Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile
            180                 185                 190
Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile
            195                 200                 205
Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys
    210                 215                 220
Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp
225                 230                 235                 240
Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr
                245                 250                 255
Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr
            260                 265                 270
Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr
            275                 280                 285
Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr
    290                 295                 300
Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr
305                 310                 315                 320
Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala
                325                 330                 335
Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp
            340                 345                 350
Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln
            355                 360                 365
Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn
            370                 375                 380
Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu
385                 390                 395                 400
Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr
                405                 410                 415
```

Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu
            420   425   430
Arg Pro Leu
            435

<210> 7
<211> 1341
<212> DNA
<213> Synthetic Construct

<220>

<221> CDS
<222> (10)...(1329)

<400> 7
gaattcacg atg gcc aac aaa tac aat tcc gaa atc ctg aac aat atc atc 51
          Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile
            1   5   10

ctg aac ctg cgt tac aaa gac aac aat ctg atc gat ctg tct ggt tac   99
Leu Asn Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr
 15   20   25   30

ggt gct aaa gtt gaa gta tac gac ggt gtt gaa ctg aat gac aag aac   147
Gly Ala Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn
                35   40   45

cag ttc aaa ctg acc tct tcc gct aac tct aag atc cgt gtt act cag   195
Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln
            50   55   60

aat cag aac atc atc ttc aac tcc gta ttc ctg gac ttc tct gtt tcc   243
Asn Gln Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser
            65   70   75

ttc tgg att cgt atc ccg aaa tac aag aac gac ggt atc cag aat tac   291
Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr
        80   85   90

atc cac aat gaa tac acc atc atc aac tgc atg aag aat aac tct ggt   339
Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly
 95   100   105   110

tgg aag atc tcc atc cgc ggt aac cgt atc atc tgg act ctg atc gat   387
Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp
                115   120   125

atc aac ggt aag acc aaa tct gta ttc ttc gaa tac aac atc cgt gaa   435
Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu
                130   135   140

gac atc tct gaa tac atc aat cgc tgg ttc ttc gtt acc atc acc aat   483
Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn
            145   150   155

aac ctg aac aat gct aaa atc tac atc aac ggt aaa ctg gaa tct aat   531
Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn
            160   165   170

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acc gac atc aaa gac atc cgt gaa gtt atc gct aac ggt gaa atc atc    579
Thr Asp Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile
175             180             185             190

ttc aaa ctg gac ggt gac atc gat cgt acc cag ttc atc tgg atg aaa    627
Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys
            195             200             205

tac ttc tcc atc ttc aac acc gaa ctg tct cag tcc aat atc gaa gaa    675
Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu
            210             215             220

cgg tac aag atc cag tct tac tcc gaa tac ctg aaa gac ttc tgg ggt    723
Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly
            225             230             235

aat ccg ctg atg tac aac aaa gaa tac tat atg ttc aat gct ggt aac    771
Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn
            240             245             250

aag aac tct tac atc aaa ctg aag aaa gac tct ccg gtt ggt gaa atc    819
Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile
255             260             265             270

ctg act cgt tcc aaa tac aac cag aac tct aaa tac atc aac tac cgc    867
Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg
                275             280             285

gac ctg tac atc ggt gaa aag ttc atc atc cgt cgc aaa tct aac tct    915
Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser
            290             295             300

cag tcc atc aat gat gac atc gta cgt aaa gaa gac tac atc tac ctg    963
Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu
            305             310             315

gac ttc ttc aac ctg aat cag gaa tgg cgt gta tac acc tac aag tac   1011
Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr
            320             325             330

ttc aag aaa gaa gaa gaa aag ctt ttc ctg gct ccg atc tct gat tcc   1059
Phe Lys Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser
335             340             345             350

gac gaa ctc tac aac acc atc cag atc aaa gaa tac gac gaa cag ccg   1107
Asp Glu Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro
                355             360             365

acc tac tct tgc cag ctg ctg ttc aag aaa gat gaa gaa tct act gac   1155
Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp
                370             375             380

gaa atc ggt ctg atc ggt atc cac cgt ttc tac gaa tct ggt atc gta   1203
Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val
            385             390             395

ttc gaa gaa tac aaa gac tac ttc tgc atc tcc aaa tgg tac ctg aag   1251
Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys
            400             405             410
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gaa gtt aaa cgc aaa ccg tac aac ctg aaa ctg ggt tgc aat tgg cag      1299
Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln
415             420                 425                 430

ttc atc ccg aaa gac gaa ggt tgg acc gaa tagtaagaat tc                1341
Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu
                435                 440


<210> 8
<211> 440
<212> PRT
<213> Synthetic Construct

<220>


<400> 8
Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn
 1               5                  10                  15
Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala
            20                  25                  30
Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe
        35                  40                  45
Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln
    50                  55                  60
Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp
65                  70                  75                  80
Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His
                85                  90                  95
Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys
            100                 105                 110
Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn
        115                 120                 125
Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile
    130                 135                 140
Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu
145                 150                 155                 160
Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp
                165                 170                 175
Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys
            180                 185                 190
Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe
        195                 200                 205
Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr
    210                 215                 220
Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro
225                 230                 235                 240
Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn
                245                 250                 255
Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr
            260                 265                 270
Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu
        275                 280                 285
Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser
    290                 295                 300
Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe
305                 310                 315                 320
Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys
                325                 330                 335
Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu
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                340                    345                    350
Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr
        355                    360                    365
Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile
    370                    375                    380
Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu
385                    390                    395                    400
Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val
                405                    410                    415
Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile
                420                    425                    430
Pro Lys Asp Glu Gly Trp Thr Glu
            435                    440


<210> 9
<211> 1371
<212> DNA
<213> Synthetic Construct

<220>

<221> CDS
<222> (10)...(1359)


<400> 9
gaattcacg atg acc atc cca ttc aac atc ttc tcc tac acc aac aac tcc 51
          Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser
          1                   5                        10

ctg ttg aag gac atc atc aac gag tac ttc aac aac atc aac gac tcc   99
Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser
 15                   20                   25                   30

aag atc ctg tcc ctg cag aac cgt aag aac acc ttg gtc gac acc tcc  147
Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser
                 35                   40                   45

ggt tac aac gcc gag gtc tcc gag gag ggt gac gtc cag ctg aac cca  195
Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro
             50                   55                   60

atc ttc cca ttc gac ttc aag ctg ggt tcc tcc ggt gag gac aga ggt  243
Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly
         65                   70                   75

aag gtc atc gtc acc cag aac gag aac atc gtc tac aac tcc atg tac  291
Lys Val Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr
     80                   85                   90

gag tcc ttc tcc atc tcc ttc tgg atc aga atc aac aag tgg gtc tcc  339
Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser
 95                   100                  105                  110

aac ttg cca ggt tac acc atc atc gac tcc gtc aag aac aac tcc ggt  387
Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly
                 115                  120                  125

tgg tcc atc ggt atc atc tcc aac ttc ctg gtc ttc acc ctg aag cag  435
Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln
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                130                     135                        140

aac gag gac tcc gag cag tcc atc aac ttc tcc tac gac atc tcc aac    483
Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn
        145                     150                     155

aac gct cct ggt tac aac aag tgg ttc ttc gtc acc gtc acc aac aac    531
Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn
        160                     165                     170

atg atg ggt aac atg aag atc tac atc aac ggt aag ctg atc gac acc    579
Met Met Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr
175                     180                     185                     190

atc aag gtc aag gag ttg acc ggt atc aac ttc tcc aag acc atc acc    627
Ile Lys Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr
                195                     200                     205

ttc gag atc aac aag atc cca gac acc ggt ctg atc acc tcc gac tcc    675
Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser
                210                     215                     220

gac aac atc aac atg tgg atc cgt gac ttc tac atc ttc gcc aag gag    723
Asp Asn Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu
        225                     230                     235

ttg gac ggt aag gac atc aac atc ctg ttc aac tcc ttg cag tac acc    771
Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr
        240                     245                     250

aac gtc gtc aag gac tac tgg ggt aac gac ctg aga tac aac aag gag    819
Asn Val Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu
255                     260                     265                     270

tac tac atg gtc aac atc gac tac ttg aac aga tac atg tac gcc aac    867
Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn
                275                     280                     285

tcc aga cag atc gtc ttc aac acc aga cgt aac aac aac gac ttc aac    915
Ser Arg Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn
                290                     295                     300

gag ggt tac aag atc atc atc aag cgt atc aga ggt aac acc aac gac    963
Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp
        305                     310                     315

acc aga gtc aga ggt ggt gac atc ctg tac ttc gac atg act atc aac    1011
Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn
        320                     325                     330

aac aag gcc tac aac ctg ttc atg aag aac gag acc atg tac gcc gac    1059
Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp
335                     340                     345                     350

aac cac tcc acc gag gac atc tac gcc atc ggt ctg cgt gag cag acc    1107
Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr
                355                     360                     365

aag gac atc aac gac aac atc atc ttc cag atc cag cca atg aac aac    1155
Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn
        370                     375                     380
```

```
act tac tac tac gct tcc cag atc ttc aag tcc aac ttc aac ggt gag    1203
Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu
        385             390             395

aac atc tcc ggt atc tgt tcc atc ggt acc tac aga ttc cgt ctg ggt    1251
Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly
    400             405             410

ggt gac tgg tac aga cac aac tac ttg gtt cca act gtc aag cag ggt    1299
Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly
415             420             425             430

aac tac gcc tcc ttg ctg gag tcc act tcc acc cac tgg gga ttc gtc    1347
Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val
                435             440             445

cca gtc tcc gag taataggaat tc                                      1371
Pro Val Ser Glu
            450


<210> 10
<211> 450
<212> PRT
<213> Synthetic Construct

<220>


<400> 10
Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu
1               5               10              15
Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser Lys Ile
            20              25              30
Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser Gly Tyr
        35              40              45
Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro Ile Phe
    50              55              60
Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly Lys Val
65              70              75              80
Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr Glu Ser
                85              90              95
Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser Asn Leu
            100             105             110
Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly Trp Ser
        115             120             125
Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln Asn Glu
    130             135             140
Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn Asn Ala
145             150             155             160
Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn Met Met
                165             170             175
Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr Ile Lys
            180             185             190
Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr Phe Glu
        195             200             205
Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser Asp Asn
    210             215             220
Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu Leu Asp
225             230             235             240
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```
Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr Asn Val
            245                 250                 255
Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr
            260                 265                 270
Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn Ser Arg
            275                 280                 285
Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn Glu Gly
        290                 295                 300
Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp Thr Arg
305                 310                 315                 320
Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn Asn Lys
            325                 330                 335
Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp Asn His
            340                 345                 350
Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr Lys Asp
            355                 360                 365
Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn Thr Tyr
        370                 375                 380
Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu Asn Ile
385                 390                 395                 400
Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly Gly Asp
            405                 410                 415
Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly Asn Tyr
            420                 425                 430
Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val Pro Val
            435                 440                 445
Ser Glu
    450


<210> 11
<211> 1374
<212> DNA
<213> Synthetic Construct

<220>
<221> CDS
<222> (10)...(1362)

<400> 11
gaattcacg atg cgt ttg aag gct aag gtc aac gag tcc ttc gag aac acc  51
          Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr
           1               5                   10


atg cca ttc aac atc ttc tcc tac acc aac aac tcc ttg ttg aag gac  99
Met Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp
 15                  20                  25                  30


atc atc aac gag tac ttc aac tcc atc aac gac tcc aag atc ttg tcc  147
Ile Ile Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser
                35                  40                  45


ttg cag aac aag aag aac gcc ttg gtc gac acc tcc ggt tac aac gcc  195
Leu Gln Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala
                50                  55                  60


gag gtc aga gtc ggt gac aac gtc cag ttg aac acc atc tac acc aac  243
Glu Val Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn
                65                  70                  75


gac ttc aag ttg tcc tct tcc ggt gac aag atc atc gtc aac ttg aac  291
```

```
Asp Phe Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn
    80                  85                  90

aac aac atc ttg tac tcc gcc atc tac gag aac tcc tct gtc tcc ttc    339
Asn Asn Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe
95                  100                 105                 110

tgg atc aag atc tcc aag gac ttg acc aac tcc cac aac gag tac acc    387
Trp Ile Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr
                115                 120                 125

atc atc aac tcc atc gag cag aac tcc ggt tgg aag ttg tgt atc cgt    435
Ile Ile Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg
                130                 135                 140

aac ggt aac atc gag tgg atc ttg cag gac gtc aac cgt aag tac aag    483
Asn Gly Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys
            145                 150                 155

tcc ttg atc ttc gac tac tcc gag tcc ttg tcc cac acc ggt tac acc    531
Ser Leu Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr
    160                 165                 170

aac aag tgg ttc ttc gtc acc atc acc aac aac atc atg ggt tac atg    579
Asn Lys Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met
175                 180                 185                 190

aag ttg tac atc aac ggt gag ttg aag cag tcc cag aag atc gag gac    627
Lys Leu Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp
                195                 200                 205

ctg gac gag gtc aag ctg gac aag acc atc gtc ttc ggt atc gac gag    675
Leu Asp Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu
            210                 215                 220

aac atc gac gag aac cag atg ttg tgg att cgt gac ttc aac atc ttc    723
Asn Ile Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe
        225                 230                 235

tcc aag gag ctg tcc aac gag gac atc aac atc gtc tac gag ggt cag    771
Ser Lys Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln
    240                 245                 250

atc ctg agg aac gtc atc aag gac tac tgg ggt aac cca ctg aag ttc    819
Ile Leu Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe
255                 260                 265                 270

gac acc gag tac tac atc atc aac gac aac tac atc gac cgt tac atc    867
Asp Thr Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile
                275                 280                 285

gcc cca gag tcc aac gtc ctg gtc ctg gtc cag tac cct gac ctg tcc    915
Ala Pro Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Leu Ser
            290                 295                 300

aag ctg tac acc ggt aac cct atc acc atc aag tcc gtc tcc gac aag    963
Lys Leu Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys
        305                 310                 315

aac cct tac tcc cgt atc ctg aac ggt gac aac atc atc ctg cac atg    1011
Asn Pro Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met
```

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ctg tac aac tcc cgt aag tac atg atc atc cgt gac acc gac acc atc   1059
Leu Tyr Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile
335             340             345             350

tac gcc acc cag ggt ggt gag tgt tcc cag aac tgt gtc tac gcc ctg   1107
Tyr Ala Thr Gln Gly Gly Glu Cys Ser Gln Asn Cys Val Tyr Ala Leu
            355             360             365

aag ctg cag tcc aac ctg ggt aac tac ggt atc ggt atc ttc tcc atc   1155
Lys Leu Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile
            370             375             380

aag aac atc gtc tcc aag aac aag tac tgc tcc cag atc ttc tcc tcc   1203
Lys Asn Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser
            385             390             395

ttc cgt gag aac acc atg ctg ctg gcc gac atc tac aag cct tgg cgt   1251
Phe Arg Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg
    400             405             410

ttc tcc ttc aag aac gcc tac act cct gtc gcc gtc acc aac tac gag   1299
Phe Ser Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu
415             420             425             430

acc aag ctg ctg tcc acc tcc tcc ttc tgg aag ttc atc tcc cgt gac   1347
Thr Lys Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp
            435             440             445

cca ggt tgg gtc gag taataggaat tc                                 1374
Pro Gly Trp Val Glu
            450
```

<210> 12
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12

```
Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr Met Pro
 1               5                   10                  15
Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile
            20                  25                  30
Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln
        35                  40                  45
Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val
    50                  55                  60
Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn Asp Phe
65                  70                  75                  80
Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn Asn Asn
                85                  90                  95
Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile
            100                 105                 110
Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile
        115                 120                 125
Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly
```

```
        130                    135                    140
Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys Ser Leu
145                    150                    155                    160
Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr Asn Lys
                  165                    170                    175
Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met Lys Leu
                  180                    185                    190
Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp Leu Asp
              195                    200                    205
Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile
          210                    215                    220
Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser Lys
225                    230                    235                    240
Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln Ile Leu
                  245                    250                    255
Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe Asp Thr
                  260                    265                    270
Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile Ala Pro
              275                    280                    285
Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Leu Ser Lys Leu
          290                    295                    300
Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys Asn Pro
305                    310                    315                    320
Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met Leu Tyr
                  325                    330                    335
Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile Tyr Ala
              340                    345                    350
Thr Gln Gly Gly Glu Cys Ser Gln Asn Cys Val Tyr Ala Leu Lys Leu
          355                    360                    365
Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile Lys Asn
      370                    375                    380
Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser Phe Arg
385                    390                    395                    400
Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg Phe Ser
                  405                    410                    415
Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu Thr Lys
              420                    425                    430
Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp Pro Gly
          435                    440                    445
Trp Val Glu
450
```

<210> 13
<211> 1400
<212> DNA
<213> Synthetic Construct

<220>
<221> CDS
<222> (10)...(1356)

<400> 13
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gaattcacc atg gga gag agt cag caa gaa cta aat tct atg gta act gat   51
          Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp
            1               5                     10

acc cta aat aat agt att cct ttt aag ctt tct tct tat aca gat gat   99
Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp
 15                  20                    25                    30
```

```
aaa att tta att tcc tac ttc aac aag ttc ttc aag aga att aag tct    147
Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser
                35                  40                  45

tct tcc gtt tta aac atg aga tac aag aat gat aaa tac gtc gac act    195
Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr
            50                  55                  60

tcc ggt tac gac tcc aat atc aac att aac ggt gac gtg tac aag tac    243
Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr
        65                  70                  75

cca act aac aaa aac caa ttc ggt atc tac aac gac aag ctt tcc gag    291
Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser Glu
        80                  85                  90

gtc aac atc tct caa aac gac tac att atc tac gac aac aag tac aag    339
Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys
95                  100                 105                 110

aac ttc tct att tct ttc tgg gtc agg att cct aac tac gac aac aag    387
Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys
                115                 120                 125

atc gtc aac gtt aac aac gag tac act atc atc aac tgt atg aga gac    435
Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp
            130                 135                 140

aac aac tcc ggt tgg aag gtc tct ctt aac cac aac gag atc att tgg    483
Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp
        145                 150                 155

acc ttg caa gac aac gca ggt att aac caa aag tta gca ttc aac tac    531
Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr
        160                 165                 170

ggt aac gca aac ggt att tct gac tac atc aac aag tgg att ttc gtc    579
Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val
175                 180                 185                 190

act atc act aac gac aga tta ggt gac tct aag ctt tac att aac ggt    627
Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly
                195                 200                 205

aac tta atc gac caa aag tcc att tta aac tta ggt aac att cac gtt    675
Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val
            210                 215                 220

tct gac aac atc tta ttc aag atc gtt aac tgc agt tac acc aga tac    723
Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr
        225                 230                 235

att ggc att aga tac ttc aac att ttc gac aag gag tta gac gag acc    771
Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr
        240                 245                 250

gag att caa act tta tac agc aac gaa cct aac acc aat att ttg aag    819
Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys
255                 260                 265                 270

gac ttc tgg ggt aac tac ttg ctt tac gac aag gaa tac tac tta tta    867
```

```
Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu
        275                 280                 285

aac gtg tta aag cca aac aac ttc att gat agg aga aag gat tct act      915
Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr
            290                 295                 300

tta agc att aac aac atc aga agc act att ctt tta gct aac aga tta      963
Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu
            305                 310                 315

tac tct ggt atc aag gtt aag atc caa aga gtt aac aac tct tct act     1011
Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr
            320                 325                 330

aac gat aac ctt gtt aga aag aac gat cag gtc tat att aac ttc gtc     1059
Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val
335                 340                 345                 350

gct agc aag act cac tta ttc cca tta tat gct gat acc gct acc acc     1107
Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr
                355                 360                 365

aac aag gag aag acc atc aag atc tcc tcc tct ggc aac aga ttt aac     1155
Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn
            370                 375                 380

caa gtc gtc gtt atg aac tcc gtc ggt aac aac tgt acc atg aac ttt     1203
Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe
            385                 390                 395

aaa aat aat aat gga aat aat att ggg ttg tta ggt ttc aag gca gat     1251
Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp
    400                 405                 410

act gta gtt gct agt act tgg tat tat acc cac atg aga gat cac acc     1299
Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr
415                 420                 425                 430

aac agc aat gga tgt ttt tgg aac ttt att tct gaa gaa cat gga tgg     1347
Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp
                435                 440                 445

caa gaa aaa taatagggat ccgcggccgc acgcgtcccg ggactagtga            1396
Gln Glu Lys


attc                                                               1400

<210> 14
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14
Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp Thr Leu
 1               5                   10                  15
Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp Lys Ile
```

```
                  20                      25                      30
    Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser Ser Ser
        35                      40                      45
    Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr Ser Gly
        50                      55                      60
    Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr Pro Thr
    65                      70                      75                      80
    Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser Glu Val Asn
                        85                      90                      95
    Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys Asn Phe
                        100                     105                     110
    Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys Ile Val
                        115                     120                     125
    Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp Asn Asn
        130                     135                     140
    Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp Thr Leu
    145                     150                     155                     160
    Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr Gly Asn
                        165                     170                     175
    Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile
                        180                     185                     190
    Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly Asn Leu
                        195                     200                     205
    Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val Ser Asp
        210                     215                     220
    Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr Ile Gly
    225                     230                     235                     240
    Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr Glu Ile
                        245                     250                     255
    Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys Asp Phe
                        260                     265                     270
    Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu Asn Val
                        275                     280                     285
    Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr Leu Ser
        290                     295                     300
    Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu Tyr Ser
    305                     310                     315                     320
    Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr Asn Asp
                        325                     330                     335
    Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val Ala Ser
                        340                     345                     350
    Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr Asn Lys
        355                     360                     365
    Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn Gln Val
        370                     375                     380
    Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe Lys Asn
    385                     390                     395                     400
    Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp Thr Val
                        405                     410                     415
    Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr Asn Ser
                        420                     425                     430
    Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp Gln Glu
                        435                     440                     445
    Lys
```

<210> 15
<211> 1317
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (10)...(1305)

<400> 15
gaattcacg atg tcc tac acc aac gac aag atc ctg atc ttg tac ttc aac 51
          Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn
           1   5   10

aag ctg tac aag aag atc aag gac aac tcc atc ttg gac atg aga tac 99
Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr
 15   20   25   30

gaa aac aat aag ttc atc gac atc tcc ggt tac ggt tcc aac atc tcc 147
Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser
            35   40   45

atc aac ggt gac gtc tac atc tac tcc acc aat aga aac cag ttc gga 195
Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly
          50   55   60

atc tac tcc tcc aag cct tcc gag gtc aac atc gct cag aac aac gac 243
Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp
        65   70   75

atc atc tac aac gga aga tac cag aac ttc tcc atc tcc ttc tgg gtc 291
Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val
   80   85   90

cgt atc cca aag tac ttc aac aag gtc aac ctg aat aac gag tac acc 339
Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr
 95   100   105   110

atc atc gac tgc atc cgt aac aat aac tcc gga tgg aag atc tcc ctg 387
Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu
          115   120   125

aac tac aac aag atc atc tgg acc ctg cag gac acc gcc ggt aac aat 435
Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn
        130   135   140

cag aag ttg gtc ttc aac tac acc cag atg atc tcc atc tcc gac tac 483
Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr
      145   150   155

atc aac aag tgg atc ttc gtc acc atc acc aat aac cgt ttg gga aac 531
Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn
   160   165   170

tcc aga atc tac atc aac ggt aac ttg atc gac gag aag tcc atc tcc 579
Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser
175   180   185   190

aac ttg ggt gac atc cac gtc tcc gac aac att ttg ttc aag atc gtc 627
Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val
          195   200   205

ggt tgt aac gac acc cgt tac gtc ggg atc cgt tac ttc aaa gtc ttc 675

```
Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe
            210                 215                 220

gac act gag ttg ggt aag acc gag atc gag acc ttg tac tcc gac gag   723
Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu
        225                 230                 235

cct gac cca tcc atc ctg aag gac ttc tgg ggt aac tac ctg ctg tac   771
Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr
        240                 245                 250

aac aaa cgt tac tac ttg ctg aac ttg ttg cgt acc gac aag tcc atc   819
Asn Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile
255                 260                 265                 270

acc cag aac tcc aac ttc ttg aac atc aac cag cag aga ggt gtc tac   867
Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr
                275                 280                 285

cag aag cca aac atc ttc tcc aac acc aga ttg tac acc gga gtc gag   915
Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu
            290                 295                 300

gtc att atc aga aag aac gga tct act gat att tcc aac acc gat aac   963
Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn
        305                 310                 315

ttc gtc aga aag aac gat ctg gct tac atc aac gtt gtc gac aga gat   1011
Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp
        320                 325                 330

gtc gaa tac cgt ctg tac gcc gat atc tct atc gcc aaa cct gaa aag   1059
Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys
335                 340                 345                 350

atc atc aag ctg atc cgt acc tct aac tct aac aac tct ctg gga caa   1107
Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln
                355                 360                 365

atc atc gtc atg gac tcc atc ggt aat aac tgt acc atg aac ttc cag   1155
Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln
            370                 375                 380

aac aac aac ggt gga aac atc ggt ttg ttg ggt ttc cac tcc aac aac   1203
Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn
        385                 390                 395

ttg gtc gct tcc tcc tgg tac tac aac aac atc cgt aag aac acc tcc   1251
Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser
        400                 405                 410

tcc aac ggt tgc ttc tgg tcc ttc atc tcc aag gag cac ggt tgg cag   1299
Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln
415                 420                 425                 430

gag aac taataggaat tc                                             1317
Glu Asn
```

<210> 16

<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16
Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu
1   5   10   15
Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn
                20   25   30
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn
            35   40   45
Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr
        50   55   60
Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile
65   70   75   80
Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile
                85   90   95
Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile
                100   105   110
Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr
            115   120   125
Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys
        130   135   140
Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn
145   150   155   160
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg
                165   170   175
Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu
            180   185   190
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys
        195   200   205
Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr
        210   215   220
Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp
225   230   235   240
Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
                245   250   255
Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln
            260   265   270
Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys
        275   280   285
Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile
        290   295   300
Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val
305   310   315   320
Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu
                325   330   335
Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile
            340   345   350
Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
        355   360   365
Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn
        370   375   380
Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val
385   390   395   400
Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn
                405   410   415
Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn

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<210> 17
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (10)...(1356)

<400> 17
gaattcacg atg aag gac acc atc ctg atc cag gtc ttc aac aac tac atc  51
          Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile
            1               5                  10

tcc aac atc tcc tcc aac gcc atc ctg tcc ctg tcc tac cgt ggt ggt  99
Ser Asn Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly
 15                  20                  25                  30

cgt ctg atc gac tcc tcc ggt tac gga gcc acc atg aac gtc ggt tcc  147
Arg Leu Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser
                 35                  40                  45

gac gtc atc ttc aac gac atc ggt aac ggt cag ttc aag ctg aac aac  195
Asp Val Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn
                 50                  55                  60

tcc gag aac tcc aac atc acc gcc cac cag tcc aag ttc gtc gtc tac  243
Ser Glu Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr
             65                  70                  75

gac tcc atg ttc gac aac ttc tcc atc aac ttc tgg gtc cgt acc cca  291
Asp Ser Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro
         80                  85                  90

aag tac aac aac aac gac atc cag acc tac ctg cag aac gag tac acc  339
Lys Tyr Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr
 95                  100                 105                 110

atc atc tcc tgt atc aag aac gac tcc ggt tgg aag gtc tcc atc aag  387
Ile Ile Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys
                 115                 120                 125

gga aac cgt atc atc tgg acc ctg atc gac gtc aac gcc aag tcc aag  435
Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys
             130                 135                 140

tcc atc ttc ttc gag tac tcc atc aag gac aac atc tcc gac tac atc  483
Ser Ile Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile
         145                 150                 155

aac aag tgg ttc tcc atc acc atc acc aac gac cgt ctg ggt aac gcc  531
Asn Lys Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala
 160                 165                 170

aac atc tac atc aac ggt tcc ctg aag aag tcc gag aag atc ctg aac  579
Asn Ile Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn
```

```
ctg gac cgt atc aac tcc tcc aac gac atc gac ttc aag ctg atc aac    627
Leu Asp Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn
                195                 200                 205

tgt acc gac acc acc aag ttc gtc tgg atc aag gac ttc aac atc ttc    675
Cys Thr Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe
                210                 215                 220

ggt cgt gag ctg aac gcc acc gag gtc tcc tcc ctg tac tgg atc cag    723
Gly Arg Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln
            225                 230                 235

tcc tcc acc aac acc ctg aag gac ttc tgg gga aac cca ctg cgt tac    771
Ser Ser Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr
            240                 245                 250

gac acc cag tac tac ctg ttc aac cag ggt atg cag aac atc tac atc    819
Asp Thr Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile
255                 260                 265                 270

aag tac ttc tcc aag gcc tcc atg ggt gag acc gcc cct cgt acc aac    867
Lys Tyr Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn
                275                 280                 285

ttc aac aac gcc gcc atc aac tac cag aac ctg tac ctg ggt ctg cgt    915
Phe Asn Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg
            290                 295                 300

ttc atc atc aag aag gcc tcc aac tcc cgt aac atc aac aac gac aac    963
Phe Ile Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn
            305                 310                 315

atc gtc cgt gag ggt gac tac atc tac ctg aac atc gac aac atc tcc   1011
Ile Val Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser
            320                 325                 330

gac gag tcc tac cgt gtc tac gtc ctg gtc aac tcc aag gag atc cag   1059
Asp Glu Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln
335                 340                 345                 350

acc cag ctg ttc ctg gcc cca atc aac gac gac cct acc ttc tac gac   1107
Thr Gln Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp
                355                 360                 365

gtc ctg cag atc aag aag tac tac gag aag acc acc tac aac tgt cag   1155
Val Leu Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln
            370                 375                 380

atc ctg tgc gag aag gac acc aag acc ttc gga ctg ttc ggt atc ggt   1203
Ile Leu Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly
            385                 390                 395

aag ttc gtc aag gac tac ggt tac gtc tgg gac acc tac gac aac tac   1251
Lys Phe Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr
            400                 405                 410

ttc tgt atc tcc cag tgg tac ctg cgt cgt atc tcc gag aac atc aac   1299
Phe Cys Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn
415                 420                 425                 430
```

```
aag ctg cgt ctg gga tgt aac tgg cag ttc atc cca gtc gac gag ggt      1347
Lys Leu Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly
                435                 440                 445

tgg acc gag taataggaat tc                                            1368
Trp Thr Glu
```


<210> 18
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18
```
Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile Ser Asn
 1               5                  10                  15
Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly Arg Leu
            20                  25                  30
Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser Asp Val
        35                  40                  45
Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn Ser Glu
    50                  55                  60
Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr Asp Ser
65                  70                  75                  80
Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro Lys Tyr
                85                  90                  95
Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr Ile Ile
            100                 105                 110
Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys Gly Asn
        115                 120                 125
Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys Ser Ile
    130                 135                 140
Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile Asn Lys
145                 150                 155                 160
Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala Asn Ile
                165                 170                 175
Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn Leu Asp
            180                 185                 190
Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn Cys Thr
        195                 200                 205
Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe Gly Arg
    210                 215                 220
Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln Ser Ser
225                 230                 235                 240
Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr
                245                 250                 255
Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile Lys Tyr
            260                 265                 270
Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn Phe Asn
        275                 280                 285
Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg Phe Ile
    290                 295                 300
Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn Ile Val
305                 310                 315                 320
Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser Asp Glu
                325                 330                 335
```

```
Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln Thr Gln
            340             345             350
Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp Val Leu
            355             360             365
Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln Ile Leu
            370             375             380
Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly Lys Phe
385             390             395             400
Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr Phe Cys
            405             410             415
Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn Lys Leu
            420             425             430
Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly Trp Thr
            435             440             445
Glu
```

<210> 19
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (1)...(1239)

```
<400> 19
atg gct ctg aac gac ctg tgc atc aaa gtt aac aac tgg gac ctg ttc    48
Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe
1               5               10              15

ttc tcc ccg tct gaa gac aac ttc act aac gac ctg aac aaa ggc gaa    96
Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu
                20              25              30

gaa atc acc tcc gac act aac atc gaa gct gct gaa gaa aac atc tct   144
Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser
            35              40              45

ctg gac ctg atc cag cag tac tac ctg act ttc aac ttc gac aac gaa   192
Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu
        50              55              60

ccg gaa aac atc tcc atc gaa aac ctg tct tcc gac atc atc ggt cag   240
Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln
65              70              75              80

ctg gaa ctg atg ccg aac atc gaa cgc ttc ccg aac ggc aag aaa tac   288
Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr
                85              90              95

gaa ctg gac aaa tac acc atg ttc cac tac ctg cgt gct cag gaa ttc   336
Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe
                100             105             110

gaa cac ggt aaa tct cgt atc gct ctg act aac tcc gtt aac gaa gct   384
Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala
            115             120             125
```

```
ctg ctg aac ccg tct cgc gtt tac acc ttc ttc tct tcc gac tac gtt    432
Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val
    130             135             140

aag aaa gtt aac aaa gct act gaa gct gct atg ttc ctg ggt tgg gtt    480
Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val
145             150             155             160

gaa cag ctg gtt tac gac ttc acc gac gaa act tct gaa gtt tcc acc    528
Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr
            165             170             175

act gac aaa atc gct gac atc act atc atc atc ccg tac atc ggc ccg    576
Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro
            180             185             190

gct ctg aac atc ggt aac atg ctg tac aaa gac gac ttc gtt ggt gct    624
Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala
        195             200             205

ctg atc ttc tct ggc gct gtt atc ctg ctg gaa ttc atc ccg gaa atc    672
Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile
        210             215             220

gct atc ccg gtt ctg ggt acc ttc gct ctg gtt tcc tac atc gct aac    720
Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn
225             230             235             240

aaa gtt ctg act gtt cag acc atc gac aac gct ctg tct aaa cgt aac    768
Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn
            245             250             255

gaa aaa tgg gac gaa gtt tac aaa tac atc gtt act aac tgg ctg gct    816
Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala
            260             265             270

aaa gtt aac act cag atc gac ctg atc cgt aag aag atg aaa gaa gct    864
Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala
        275             280             285

ctg gaa aac cag gct gaa gct act aaa gct atc atc aac tac cag tac    912
Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr
        290             295             300

aac cag tac acc gaa gaa gaa aag aac aac atc aac ttc aac atc gat    960
Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp
305             310             315             320

gac ctg tcc tct aaa ctg aac gaa tcc atc aac aaa gct atg atc aac    1008
Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn
            325             330             335

atc aac aaa ttc ctg aac cag tgc tct gtt tcc tac ctg atg aac tct    1056
Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser
            340             345             350

atg atc ccg tac ggc gtt aaa cgc ctg gaa gac ttc gac gct tcc ctg    1104
Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu
        355             360             365
```

```
aaa gac gct ctg ctg aaa tac atc cgt gac aac tac ggt act ctg atc    1152
Lys Asp Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile
    370             375             380

ggc cag gtt gac cgt ctg aaa gac aag gtt aac aac acc ctg tct act    1200
Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr
385             390             395             400

gac atc ccg ttc cag ctg tcc aaa tac gtt gac aac cag taa            1242
Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln
            405             410
```

<210> 20
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 20
```
Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe
1               5                   10                  15
Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu
            20                  25                  30
Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser
        35                  40                  45
Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu
    50                  55                  60
Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln
65                  70                  75                  80
Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr
                85                  90                  95
Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe
            100                 105                 110
Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala
        115                 120                 125
Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val
    130                 135                 140
Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val
145                 150                 155                 160
Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr
                165                 170                 175
Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro
            180                 185                 190
Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala
        195                 200                 205
Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile
    210                 215                 220
Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn
225                 230                 235                 240
Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn
                245                 250                 255
Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala
            260                 265                 270
Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala
        275                 280                 285
Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr
    290                 295                 300
Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp
```

```
         305                        310                        315                        320
Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn
                      325                        330                        335
Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser
                  340                        345                        350
Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu
              355                        360                        365
Lys Asp Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile
          370                        375                        380
Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr
385                        390                        395                        400
Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln
                      405                        410


<210> 21
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (1)...(1239)

<400> 21
atg gct cca gga atc tgt atc gac gtc gac aac gag gac ttg ttc ttc      48
Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe
1                   5                      10                      15

atc gct gac aag aac tcc ttc tcc gac gac ttg tcc aag aac gag aga      96
Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg
                20                      25                      30

atc gag tac aac acc cag tcc aac tac atc gag aac gac ttc cca atc     144
Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile
            35                      40                      45

aac gag ttg atc ttg gac acc gac ttg atc tcc aag atc gag ttg cca     192
Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro
        50                      55                      60

tcc gag aac acc gag tcc ttg act gac ttc aac gtc gac gtc cca gtc     240
Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val
65                      70                      75                      80

tac gag aag caa cca gct atc aag aag att ttc acc gac gag aac acc     288
Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr
                85                      90                      95

atc ttc caa tac ctg tac tct cag acc ttc cct ttg gac atc aga gac     336
Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp
                100                        105                        110

atc tcc ttg acc tct tcc ttc gac gac gcc ctg ctg ttc tcc aac aag     384
Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys
            115                        120                        125

gtc tac tcc ttc ttc tcc atg gac tac atc aag act gct aac aag gtc     432
Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val
```

```
gtc gag gcc ggt ttg ttc gct ggt tgg gtc aag cag atc gtc aac gat    480
Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp
145             150             155             160

ttc gtc atc gag gct aac aag tcc aac acc atg gac aag att gcc gac    528
Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp
                165             170             175

atc tcc ttg att gtc cca tac atc ggt ttg gcc ttg aac gtc ggt aac    576
Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn
            180             185             190

gag acc gcc aag ggt aac ttc gag aac gct ttc gag atc gct ggt gcc    624
Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala
            195             200             205

tcc atc ttg ttg gag ttc atc cca gag ttg ttg atc cca gtc gtc ggt    672
Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly
            210             215             220

gcc ttc ttg ttg gag tcc tac atc gac aac aag aac aag atc atc aag    720
Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys
225             230             235             240

acc atc gac aac gct ttg acc aag aga aac gag aag tgg tcc gac atg    768
Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met
                245             250             255

tac ggt ttg atc gtc gcc caa tgg ttg tcc acc gtc aac acc caa ttc    816
Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe
            260             265             270

tac acc atc aag gag ggt atg tac aag gcc ttg aac tac cag gcc caa    864
Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln
            275             280             285

gct ttg gag gag atc atc aag tac aga tac aac atc tac tcc gag aag    912
Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys
290             295             300

gag aag tcc aac att aac atc gac ttc aac gac atc aac tcc aag ctg    960
Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu
305             310             315             320

aac gag ggt att aac cag gcc atc gac aac atc aac aac ttc atc aac    1008
Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn
                325             330             335

ggt tgt tcc gtc tcc tac ttg atg aag aag atg att cca ttg gcc gtc    1056
Gly Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val
            340             345             350

gag aag ttg ttg gac ttc gac aac acc ctg aag aag aac ttg ttg aac    1104
Glu Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn
            355             360             365

tac atc gac gag aac aag ttg tac ttg atc ggt tcc gct gag tac gag    1152
Tyr Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu
            370             375             380
```

```
aag tcc aag gtc aac aag tac ttg aag acc atc atg cca ttc gac ttg      1200
Lys Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu
385                 390                 395                 400

tcc atc tac acc aac gac acc atc ttg atc gag atg ttc taa            1242
Ser Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe
            405                 410


<210> 22
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22
Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe
 1               5                   10                  15
Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg
            20                  25                  30
Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile
        35                  40                  45
Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro
    50                  55                  60
Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val
65                  70                  75                  80
Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr
            85                  90                  95
Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp
            100                 105                 110
Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys
        115                 120                 125
Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val
    130                 135                 140
Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp
145                 150                 155                 160
Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp
            165                 170                 175
Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn
            180                 185                 190
Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala
        195                 200                 205
Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly
    210                 215                 220
Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys
225                 230                 235                 240
Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met
            245                 250                 255
Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe
            260                 265                 270
Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln
    275                 280                 285
Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys
    290                 295                 300
Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu
305                 310                 315                 320
Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn
            325                 330                 335
```

```
Gly Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val
            340                 345             350
Glu Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn
        355                 360             365
Tyr Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu
    370                 375             380
Lys Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu
385                 390             395                 400
Ser Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe
                405                 410


<210> 23
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (1)...(1197)

<400> 23
atg tcc ctg tac aac aag acc ctt gac tgt aga gag ctg ctg gtg aag    48
Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys
 1               5                   10                  15

aac act gac ctg cca ttc atc ggt gac atc agt gac gtg aag act gac    96
Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp
                20                  25                  30

atc ttc ctg cgt aag gac atc aac gag gag act gag gtg atc tac tac   144
Ile Phe Leu Arg Lys Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr
            35                  40                  45

cca gac aac gtg tca gta gac caa gtg atc ctc agt aag aac acc tcc   192
Pro Asp Asn Val Ser Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser
        50                  55                  60

gag cat gga caa cta gac ctg ctc tac cct agt atc gac agt gag agt   240
Glu His Gly Gln Leu Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser
65                  70                  75                  80

gag atc ctg cca ggg gag aat caa gtc ttc tac gac aac cgt acc cag   288
Glu Ile Leu Pro Gly Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln
                85                  90                  95

aac gtg gac tac ctg aac tcc tac tac tac cta gag tct cag aag ctg   336
Asn Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu
            100                 105                 110

agt gac aac gtg gag gac ttc act ttc acg cgt tca atc gag gag gct   384
Ser Asp Asn Val Glu Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala
        115                 120                 125

ctg gac aac agt gca aag gtg tac act tac ttc cct acc ctg gct aac   432
Leu Asp Asn Ser Ala Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn
    130                 135                 140

aag gtg aat gcc ggt gtg caa ggt ggt ctg ttc ctg atg tgg gca aac   480
```

```
Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn
145             150             155             160

gac gtg gtt gag gac ttc act acc aac atc ctg cgt aag gac aca ctg     528
Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu
                165             170             175

gac aag atc tca gat gtg tca gct atc atc ccc tac atc gga ccc gca     576
Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala
            180             185             190

ctg aac atc tcc aac tct gtg cgt cgt gga aac ttc act gag gca ttc     624
Leu Asn Ile Ser Asn Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe
            195             200             205

gca gtc act ggt gtc acc atc ctg ctg gag gca ttc cct gag ttc aca     672
Ala Val Thr Gly Val Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr
            210             215             220

atc cct gct ctg ggt gca ttc gtg atc tac agt aag gtc cag gag cga     720
Ile Pro Ala Leu Gly Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg
225             230             235             240

aac gag atc atc aag acc atc gac aac tgt ctg gag cag agg atc aag     768
Asn Glu Ile Ile Lys Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys
                245             250             255

aga tgg aag gac tcc tac gag tgg atg atg gga acg tgg ttg tcc agg     816
Arg Trp Lys Asp Ser Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg
            260             265             270

atc atc acc cag ttc aac aac atc tcc tac cag atg tac gac tcc ctg     864
Ile Ile Thr Gln Phe Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu
            275             280             285

aac tac cag gca ggt gca atc aag gct aag atc gac ctg gag tac aag     912
Asn Tyr Gln Ala Gly Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys
            290             295             300

aag tac tcc gga agc gac aag gag aac atc aag agc cag gtt gag aac     960
Lys Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn
305             310             315             320

ctg aag aac agt ctg gac gtc aag atc tcg gag gca atg aac aac atc     1008
Leu Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile
                325             330             335

aac aag ttc atc cga gag tgc tcc gtc acc tac ctg ttc aag aac atg     1056
Asn Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met
                340             345             350

ctg cct aag gtc atc gac gag ctg aac gag ttc gac cga aac acc aag     1104
Leu Pro Lys Val Ile Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys
            355             360             365

gca aag ctg atc aac ctg atc gac tcc cat aac atc atc ctg gtc ggt     1152
Ala Lys Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly
            370             375             380

gag gtc gac aag ctg aag gca aag gta aac aac agc ttc cag aac          1197
Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn
```

<210> 24
<211> 399
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 24
Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys
1   5   10   15
Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp
            20   25   30
Ile Phe Leu Arg Lys Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr
        35   40   45
Pro Asp Asn Val Ser Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser
    50   55   60
Glu His Gly Gln Leu Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser
65   70   75   80
Glu Ile Leu Pro Gly Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln
                85   90   95
Asn Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu
            100   105   110
Ser Asp Asn Val Glu Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala
        115   120   125
Leu Asp Asn Ser Ala Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn
    130   135   140
Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn
145   150   155   160
Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu
                165   170   175
Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala
            180   185   190
Leu Asn Ile Ser Asn Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe
            195   200   205
Ala Val Thr Gly Val Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr
    210   215   220
Ile Pro Ala Leu Gly Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg
225   230   235   240
Asn Glu Ile Ile Lys Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys
                245   250   255
Arg Trp Lys Asp Ser Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg
            260   265   270
Ile Ile Thr Gln Phe Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu
        275   280   285
Asn Tyr Gln Ala Gly Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys
    290   295   300
Lys Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn
305   310   315   320
Leu Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile
                325   330   335
Asn Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met
            340   345   350
Leu Pro Lys Val Ile Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys
            355   360   365
Ala Lys Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly
    370   375   380

```
Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn
385             390             395


<210> 25
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (1)...(1158)

<400> 25
atg gcc aac tcc cgt gac gac tcc acc tgc atc aag gtc aag aac aac    48
Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
 1               5                  10                  15

aga ctg cca tac gtt gcc gac aag gac tcc atc tcc cag gag atc ttc    96
Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
             20                  25                  30

gag aac aag atc atc acc gac gag acc aac gtt caa aac tac tcc gac    144
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
         35                  40                  45

aag ttc tct ttg gac gag tcc atc ctg gac ggt cag gtc cca atc aac    192
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
     50                  55                  60

cca gag atc gtc gac cca ctg ttg cca aac gtc aac atg gag cca ttg    240
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
 65                  70                  75                  80

aac ttg cca ggt gag gag atc gtc ttc tac gac gac atc acc aag tac    288
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
                 85                  90                  95

gtc gac tac ttg aac tcc tac tac tac ttg gag tct caa aag ttg tct    336
Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
             100                 105                 110

aac aac gtc gag aac atc acc ttg acc acc tcc gtc gag gag gcc ttg    384
Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu
         115                 120                 125

ggt tac tct aac aag atc tac acc ttc ctg cca tcc ttg gct gag aag    432
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
     130                 135                 140

gtt aac aag ggt gtt caa gct ggt ttg ttc ctg aac tgg gcc aac gag    480
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
145                 150                 155                 160

gtc gtc gag gac ttc acc acc aac atc atg aag aag gac acc ctg gac    528
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
                 165                 170                 175

aag atc tcc gac gtc tcc gtc atc atc cca tac atc ggt cca gcc ttg    576
```

```
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu
            180                 185                 190

aac atc ggt aac tcc gcc ctg aga ggt aac ttc aac cag gcc ttc gcc    624
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala
            195                 200                 205

acc gcc ggt gtc gcc ttc ctg ctg gag ggt ttc cca gag ttc acc atc    672
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile
    210                 215                 220

cca gcc ctg ggt gtc ttc acc ttc tac tcc tcc atc cag gag aga gag    720
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu
225                 230                 235                 240

aag atc atc aag acc atc gag aac tgc ttg gag cag aga gtc aag aga    768
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg
            245                 250                 255

tgg aag gac tcc tac cag tgg atg gtt tcc aac tgg ctg tcc aga atc    816
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile
            260                 265                 270

acc acc caa ttc aac cac atc aac tac cag atg tac gac tcc ctg tcc    864
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser
            275                 280                 285

tac cag gcc gac gcc atc aag gcc aag atc gac ctg gag tac aag aag    912
Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys
    290                 295                 300

tac tcc ggt tcc gac aag gag aac atc aag tcc cag gtc gag aac ctg    960
Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu
305                 310                 315                 320

aag aac tcc ttg gac gtc aag atc tcc gag gcc atg aac aac atc aac   1008
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn
            325                 330                 335

aag ttc atc cgt gag tgt tcc gtc acc tac ctg ttc aag aac atg ctg   1056
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu
            340                 345                 350

cca aag gtc atc gac gag ctg aac aag ttc gac ctg aga acc aag acc   1104
Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr
            355                 360                 365

gag ctg atc aac ctg atc gac tcc cac aac atc atc ctg gtt ggt gag   1152
Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu
    370                 375                 380

gtt gac taa                                                        1161
Val Asp
385


<210> 26
<211> 386
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Synthetic Construct

<400> 26
Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
 1   5   10   15
Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
            20   25   30
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
        35   40   45
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
    50   55   60
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
65   70   75   80
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
                85   90   95
Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
            100   105   110
Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu
        115   120   125
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
        130   135   140
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
145   150   155   160
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
                165   170   175
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu
            180   185   190
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala
        195   200   205
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile
    210   215   220
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu
225   230   235   240
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg
                245   250   255
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile
            260   265   270
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser
        275   280   285
Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys
    290   295   300
Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu
305   310   315   320
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn
                325   330   335
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu
            340   345   350
Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr
            355   360   365
Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu
        370   375   380
Val Asp
385

<210> 27
<211> 1149
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (1)...(1146)

<400> 27
```
atg tcc atc tgc atc gag atc aac aac ggt gag ctg ttc ttc gtg gct    48
Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala
1               5                   10                  15

tcc gag aac agt tac aac gat gac aac atc aac act cct aag gag att    96
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile
                20                  25                  30

gac gac acc gtc act tct aac aac aac tac gaa aac gac ctg gac cag   144
Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln
            35                  40                  45

gtc atc cta aac ttc aac tcc gag tcc gcc cct ggt ctg tcc gac gag   192
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu
        50                  55                  60

aag ctg aac ctg acc atc cag aac gac gct tac atc cca aag tac gac   240
Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp
65                  70                  75                  80

tcc aac ggt aca tcc gat atc gag cag cat gac gtt aac gag ctt aac   288
Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn
                85                  90                  95

gtc ttc ttc tac tta gac gct cag aag gtg ccc gag ggt gag aac aac   336
Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn
                100                 105                 110

gtc aat ctc acc tct tca att gac aca gcc ttg ttg gag cag cct aag   384
Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys
            115                 120                 125

atc tac acc ttc ttc tcc tcc gag ttc atc aac aac gtc aac aag cct   432
Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro
        130                 135                 140

gtg cag gcc gca ttg ttc gta agc tgg att cag cag gtg tta gta gac   480
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp
145                 150                 155                 160

ttc act act gag gct aac cag aag tcc act gtt gac aag atc gct gac   528
Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp
                165                 170                 175

atc tcc atc gtc gtc cca tac atc ggt ctg gct ctg aac atc ggc aac   576
Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn
            180                 185                 190

gag gca cag aag ggc aac ttc aag gat gcc ctt gag ttg ttg ggt gcc   624
Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala
            195                 200                 205

ggt att ttg ttg gag ttc gaa ccc gag ctg ctg atc cct acc atc ctg   672
Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu
```

```
          210                    215                    220

gtc ttc acg atc aag tcc ttc ctg ggt tcc tcc gac aac aag aac aag   720
Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys
225                 230                 235                 240

gtc att aag gcc atc aac aac gcc ctg aag gag cgt gac gag aag tgg   768
Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp
                    245                 250                 255

aag gaa gtc tat tcc ttc atc gtc tcg aac tgg atg acc aag atc aac   816
Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn
                260                 265                 270

acc cag ttc aac aag cga aag gag cag atg tac cag gct ctg cag aac   864
Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn
            275                 280                 285

cag gtc aac gcc atc aag acc atc atc gag tcc aag tac aac tcc tac   912
Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr
        290                 295                 300

acc ctg gag gag aag aac gag ctt acc aac aag tac gat atc aag cag   960
Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln
305                 310                 315                 320

atc gag aac gag ctg aac cag aag gtc tcc atc gcc atg aac aac atc   1008
Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile
                    325                 330                 335

gac agg ttc ctg acc gag tcc tcc atc tcc tac ctg atg aag ctc atc   1056
Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile
            340                 345                 350

aac gag gtc aag atc aac aag ctg cga gag tac gac gag aat gtc aag   1104
Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys
        355                 360                 365

acg tac ctg ctg aac tac atc atc cag cac gga tcc atc ctg           1146
Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu
        370                 375                 380

taa                                                               1149

<210> 28
<211> 382
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 28
Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala
 1               5                  10                  15
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile
                20                  25                  30
Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln
            35                  40                  45
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu
        50                  55                  60
```

```
Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp
65                  70                  75                  80
Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn
                85                  90                  95
Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn
                100                 105                 110
Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys
            115                 120                 125
Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro
        130                 135                 140
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp
145                 150                 155                 160
Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp
                165                 170                 175
Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn
                180                 185                 190
Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala
                195                 200                 205
Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu
        210                 215                 220
Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys
225                 230                 235                 240
Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp
                245                 250                 255
Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn
                260                 265                 270
Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn
        275                 280                 285
Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr
        290                 295                 300
Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln
305                 310                 315                 320
Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile
                325                 330                 335
Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile
        340                 345                 350
Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys
        355                 360                 365
Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu
        370                 375                 380
```

<210> 29
<211> 1227
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (1)...(1224)

<400> 29
```
atg gcc cca cca cgt ctg tgt att aga gtc aac aac tca gaa tta ttc    48
Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
 1               5                   10                  15

ttt gtc gct tcc gag tca agc tac aac gag aac gat att aac aca cct    96
Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
                20                  25                  30
```

```
aaa gag att gac gat act acc aac cta aac aac aac tac cgg aac aac    144
Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn
         35                  40                  45

ttg gat gag gtt att ttg gat tac aac tca cag acc atc cct caa att    192
Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
         50                  55                  60

tcc aac cgt acc tta aac act ctt gtc caa gac aac tcc tac gtt cca    240
Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
 65                  70                  75                  80

aga tac gat tct aac ggt acc tca gag atc gag gag tat gat gtt gtt    288
Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
                 85                  90                  95

gac ttt aac gtc ttt ttc tat ttg cat gcc cag aag gtg cca gaa ggt    336
Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly
                100                 105                 110

gaa acc aac atc tca ttg act tct tcc att gat acc gcc ttg ttg gaa    384
Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu
            115                 120                 125

gag tcc aag gat atc ttc ttt tct tcg gag ttt atc gat act atc aac    432
Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu Phe Ile Asp Thr Ile Asn
        130                 135                 140

aag cct gtc aac gcc gct ctg ttc att gat tgg att agc aag gtc atc    480
Lys Pro Val Asn Ala Ala Leu Phe Ile Asp Trp Ile Ser Lys Val Ile
145                 150                 155                 160

aga gat ttt acc act gaa gct act caa aag tcc act gtt gat aag att    528
Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys Ser Thr Val Asp Lys Ile
                165                 170                 175

gct gac atc tct ttg att gtc ccc tat gtc ggt ctt gct ttg aac atc    576
Ala Asp Ile Ser Leu Ile Val Pro Tyr Val Gly Leu Ala Leu Asn Ile
            180                 185                 190

att att gag gca gaa aag ggt aac ttt gag gag gct ttt gaa ttg ttg    624
Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu Glu Ala Phe Glu Leu Leu
        195                 200                 205

gga gtt ggt att ttg ttg gag ttt gtt cca gaa ctt acc att cct gtc    672
Gly Val Gly Ile Leu Leu Glu Phe Val Pro Glu Leu Thr Ile Pro Val
        210                 215                 220

att tta gtt ttt acg atc aag tcc tac atc gat tca tac gag aac aag    720
Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile Asp Ser Tyr Glu Asn Lys
225                 230                 235                 240

aat aaa gca att aaa gct att aac aac tcc ttg atc gaa aga gag gct    768
Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser Leu Ile Glu Arg Glu Ala
                245                 250                 255

aag tgg aag gaa atc tac tca tgg att gta tca aac tgg ctt act aga    816
Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val Ser Asn Trp Leu Thr Arg
        260                 265                 270
```

```
att aac act caa ttt aac aag aga aag gag caa atg tac cag gct ctg    864
Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu
        275                 280                 285

caa aac caa gtc gat gct atc aag act gca att gaa tac aag tac aac    912
Gln Asn Gln Val Asp Ala Ile Lys Thr Ala Ile Glu Tyr Lys Tyr Asn
        290                 295                 300

aac tat act tcc gat gag aag aac aga ctt gaa tct gaa tac aat atc    960
Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu Glu Ser Glu Tyr Asn Ile
305                 310                 315                 320

aac aac att gaa gaa gag ttg aac aag aaa gtt tct ttg gct atg aag   1008
Asn Asn Ile Glu Glu Glu Leu Asn Lys Lys Val Ser Leu Ala Met Lys
                325                 330                 335

aat atc gaa aga ttt atg acc gaa tcc tct atc tct tac ttg atg aag   1056
Asn Ile Glu Arg Phe Met Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys
            340                 345                 350

ttg atc aat gag gcc aag gtt ggt aag ttg aag aag tac gat aac cac   1104
Leu Ile Asn Glu Ala Lys Val Gly Lys Leu Lys Lys Tyr Asp Asn His
            355                 360                 365

gtt aag agc gat ctg ctg aac tac att ctc gac cac aga tca atc ctg   1152
Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu Asp His Arg Ser Ile Leu
        370                 375                 380

gga gag cag aca aac gag ctg agt gat ttg gtt act tcc act ttg aac   1200
Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu Val Thr Ser Thr Leu Asn
385                 390                 395                 400

tcc tcc att cca ttt gag ctt tct taa                               1227
Ser Ser Ile Pro Phe Glu Leu Ser
                405


<210> 30
<211> 408
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 30
Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
 1               5                  10                  15
Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
            20                  25                  30
Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn
            35                  40                  45
Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
        50                  55                  60
Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
65                  70                  75                  80
Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
                85                  90                  95
Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly
            100                 105                 110
Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu
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          115                    120                    125
Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu Phe Ile Asp Thr Ile Asn
    130                    135                    140
Lys Pro Val Asn Ala Ala Leu Phe Ile Asp Trp Ile Ser Lys Val Ile
145                    150                    155                    160
Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys Ser Thr Val Asp Lys Ile
                   165                    170                    175
Ala Asp Ile Ser Leu Ile Val Pro Tyr Val Gly Leu Ala Leu Asn Ile
                   180                    185                    190
Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu Glu Ala Phe Glu Leu Leu
                   195                    200                    205
Gly Val Gly Ile Leu Leu Glu Phe Val Pro Glu Leu Thr Ile Pro Val
    210                    215                    220
Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile Asp Ser Tyr Glu Asn Lys
225                    230                    235                    240
Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser Leu Ile Glu Arg Glu Ala
                   245                    250                    255
Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val Ser Asn Trp Leu Thr Arg
                   260                    265                    270
Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu
                   275                    280                    285
Gln Asn Gln Val Asp Ala Ile Lys Thr Ala Ile Glu Tyr Lys Tyr Asn
    290                    295                    300
Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu Glu Ser Glu Tyr Asn Ile
305                    310                    315                    320
Asn Asn Ile Glu Glu Glu Leu Asn Lys Lys Val Ser Leu Ala Met Lys
                   325                    330                    335
Asn Ile Glu Arg Phe Met Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys
                   340                    345                    350
Leu Ile Asn Glu Ala Lys Val Gly Lys Leu Lys Lys Tyr Asp Asn His
    355                    360                    365
Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu Asp His Arg Ser Ile Leu
370                    375                    380
Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu Val Thr Ser Thr Leu Asn
385                    390                    395                    400
Ser Ser Ile Pro Phe Glu Leu Ser
                   405


<210> 31
<211> 1233
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (1)...(1230)

<400> 31
atg gcc aaa aat acc ggt aaa tct gaa cag tgt att att gtt aat aat      48
Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
 1               5                  10                  15

gag gat tta ttt ttc ata gct aat aaa gat agt ttt tca aaa gat tta      96
Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
              20                  25                  30

gct aaa gca gaa act ata gca tat aat aca caa aat aat act ata gaa     144
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
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aat aat ttt tct ata gat cag ttg att tta gat aat gat tta agc agt   192
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
        50                  55                  60

ggc ata gac tta cca aat gaa aac aca gaa cca ttt aca aat ttt gac   240
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
65                  70                  75                  80

gac ata gat atc cct gtg tat att aaa caa tct gct tta aaa aaa att   288
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
                85                  90                  95

ttt gtg gat gga gat agc ctt ttt gaa tat tta cat gct caa aca ttt   336
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
            100                 105                 110

cct tct aat ata gaa aat cta caa cta acg aat tca tta aat gat gct   384
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
        115                 120                 125

tta aga aat aat aat aaa gtc tat act ttt ttt tct aca aac ctt gtt   432
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val
        130                 135                 140

gaa aaa gct aat aca gtt gta ggt gct tca ctt ttt gta aac tgg gta   480
Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val
145                 150                 155                 160

aaa gga gta ata gat gat ttt aca tct gaa tcc aca caa aaa agt act   528
Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr
                165                 170                 175

ata gat aaa gtt tca gat gta tcc ata att att ccc tat ata gga cct   576
Ile Asp Lys Val Ser Asp Val Ser Ile Ile Ile Pro Tyr Ile Gly Pro
            180                 185                 190

gct ttg aat gta gga aat gaa aca gct aaa gaa aat ttt aaa aat gct   624
Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala
        195                 200                 205

ttt gaa ata ggt gga gcc gct atc tta atg gag ttt att cca gaa ctt   672
Phe Glu Ile Gly Gly Ala Ala Ile Leu Met Glu Phe Ile Pro Glu Leu
        210                 215                 220

att gta cct ata gtt gga ttt ttt aca tta gaa tca tat gta gga aat   720
Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn
225                 230                 235                 240

aaa ggg cat att att atg acg ata tcc aat gct tta aag aaa agg gat   768
Lys Gly His Ile Ile Met Thr Ile Ser Asn Ala Leu Lys Lys Arg Asp
                245                 250                 255

caa aaa tgg aca gat atg tat ggt ttg ata gta tcg cag tgg ctc tca   816
Gln Lys Trp Thr Asp Met Tyr Gly Leu Ile Val Ser Gln Trp Leu Ser
            260                 265                 270

acg gtt aat act caa ttt tat aca ata aaa gaa aga atg tac aat gct   864
Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Arg Met Tyr Asn Ala
        275                 280                 285
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tta aat aat caa tca caa gca ata gaa aaa ata ata gaa gat caa tat    912
Leu Asn Asn Gln Ser Gln Ala Ile Glu Lys Ile Ile Glu Asp Gln Tyr
    290             295             300

aat aga tat agt gaa gaa gat aaa atg aat att aac att gat ttt aat    960
Asn Arg Tyr Ser Glu Glu Asp Lys Met Asn Ile Asn Ile Asp Phe Asn
305             310             315             320

gat ata gat ttt aaa ctt aat caa agt ata aat tta gca ata aac aat   1008
Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile Asn Asn
            325             330             335

ata gat gat ttt ata aac caa tgt tct ata tca tat cta atg aat aga   1056
Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg
        340             345             350

atg att cca tta gct gta aaa aag tta aaa gac ttt gat gat aat ctt   1104
Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu
        355             360             365

aag aga gat tta ttg gag tat ata gat aca aat gaa cta tat tta ctt   1152
Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu
    370             375             380

gat gaa gta aat att cta aaa tca aaa gta aat aga cac cta aaa gac   1200
Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp
385             390             395             400

agt ata cca ttt gat ctt tca cta tat acc taa                       1233
Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr
            405             410


<210> 32
<211> 410
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 32
Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
 1               5               10              15
Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
            20              25              30
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
        35              40              45
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
    50              55              60
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
65              70              75              80
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
            85              90              95
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
        100             105             110
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
        115             120             125
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val
    130             135             140
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Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val
145             150             155             160
Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr
            165             170             175
Ile Asp Lys Val Ser Asp Val Ser Ile Ile Ile Pro Tyr Ile Gly Pro
            180             185             190
Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala
        195             200             205
Phe Glu Ile Gly Gly Ala Ala Ile Leu Met Glu Phe Ile Pro Glu Leu
    210             215             220
Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn
225             230             235             240
Lys Gly His Ile Ile Met Thr Ile Ser Asn Ala Leu Lys Lys Arg Asp
            245             250             255
Gln Lys Trp Thr Asp Met Tyr Gly Leu Ile Val Ser Gln Trp Leu Ser
            260             265             270
Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Arg Met Tyr Asn Ala
            275             280             285
Leu Asn Asn Gln Ser Gln Ala Ile Glu Lys Ile Ile Glu Asp Gln Tyr
    290             295             300
Asn Arg Tyr Ser Glu Glu Asp Lys Met Asn Ile Asn Ile Asp Phe Asn
305             310             315             320
Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile Asn Asn
            325             330             335
Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg
            340             345             350
Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu
            355             360             365
Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu
    370             375             380
Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp
385             390             395             400
Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr
            405             410


<210> 33
<211> 1314
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (10)...(1305)

<400> 33
gaattcacg atg tct tac act aac gac aaa atc ctg atc ctg tac ttc aac   51
          Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn
            1               5                   10

aaa ctg tac aaa aaa atc aaa gac aac tct atc ctg gac atg cgt tac   99
Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr
 15                 20                  25                  30

gaa aac aac aaa ttc atc gac atc tct ggc tat ggt tct aac atc tct   147
Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser
                35                  40                  45

atc aac ggt gac gtc tac atc tac tct act aac cgc aac cag ttc ggt   195
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                    Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly
                             50                      55                      60

atc tac tct tct aaa ccg tct gaa gta aac atc gct cag aac aac gac     243
Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp
         65                      70                      75

atc atc tac aac ggt cgt tac cag aac ttc tct atc tct ttc tgg gtt     291
Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val
     80                      85                      90

cgt atc ccg aaa tac ttc aac aaa gtt aac ctg aac aac gaa tac act     339
Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr
 95                     100                     105                     110

atc atc gac tgc atc cgt aac aac aac tct ggt tgg aaa atc tct ctg     387
Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu
                115                     120                     125

aac tac aac aaa atc atc tgg act ctg cag gac act gct ggt aac aac     435
Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn
                130                     135                     140

cag aaa ctg gtt ttc aac tac act cag atg atc tct atc tct gac tac     483
Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr
                145                     150                     155

att aat aaa tgg atc ttc gtt act atc act aac aac cgt ctg ggt aac     531
Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn
     160                     165                     170

tct cgt atc tac atc aac ggt aac ctg atc gat gaa aaa tct atc tct     579
Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser
175                     180                     185                     190

aac ctg ggt gac atc cac gtt tct gac aac atc ctg ttc aaa atc gtt     627
Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val
                195                     200                     205

ggt tgc aac gac acg cgt tac gtt ggt atc cgt tac ttc aaa gtt ttc     675
Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe
                210                     215                     220

gac act gaa ctg ggt aaa act gaa atc gaa act ctg tac tct gac gaa     723
Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu
                225                     230                     235

ccg gac ccg tct atc ctg aaa gac ttc tgg ggt aac tac ctg ctg tac     771
Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr
                240                     245                     250

aac aaa cgt tac tac ctg ctg aac ctg ctc cgg act gac aaa tct atc     819
Asn Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile
255                     260                     265                     270

act cag aac tct aac ttc ctg aac atc aac cag cag cgt ggt gtt tat     867
Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr
                275                     280                     285

cag aaa cct aat atc ttc tct aac act cgt ctg tac act ggt gtt gaa     915
Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu
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gtt atc atc cgt aaa aac ggt tct act gac atc tct aac act gac aac   963
Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn
        305                    310                    315

ttc gta cgt aaa aac gac ctg gct tac atc aac gtt gtt gac cgt gac  1011
Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp
        320                    325                    330

gtt gaa tac cgt ctg tac gct gac atc tct atc gct aaa ccg gaa aaa  1059
Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys
335                    340                    345                    350

atc atc aaa ctg atc cgt act tct aac tct aac aac tct ctg ggt cag  1107
Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln
                    355                    360                    365

atc atc gtt atg gac tcg atc ggt aac aac tgc act atg aac ttc cag  1155
Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln
                370                    375                    380

aac aac aac ggt ggt aac atc ggt ctg ctg ggt ttc cac tct aac aac  1203
Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn
                385                    390                    395

ctg gtt gct tct tca tgg tac tac aac aac atc cgt aaa aac act tct  1251
Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser
        400                    405                    410

tct aac ggt tgc ttc tgg tct ttc atc tct aaa gaa cac ggt tgg cag  1299
Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln
415                    420                    425                    430

gaa aac taagaattc                                                 1314
Glu Asn
```

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<210> 34
<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34
Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu
 1               5                  10                  15
Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn
            20                  25                  30
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn
            35                  40                  45
Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr
      50                  55                  60
Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile
65                  70                  75                  80
Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile
                  85                  90                  95
Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile
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          100                    105                    110
Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr
     115                    120                    125
Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys
     130                    135                    140
Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn
145                    150                    155                    160
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg
               165                    170                    175
Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu
          180                    185                    190
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys
          195                    200                    205
Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr
     210                    215                    220
Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp
225                    230                    235                    240
Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
               245                    250                    255
Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln
          260                    265                    270
Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys
          275          .         280                    285
Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile
          290                    295                    300
Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val
305                    310                    315                    320
Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu
               325                    330                    335
Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile
          340                    345                    350
Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
          355                    360                    365
Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn
     370                    375                    380
Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val
385                    390                    395                    400
Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn
               405                    410          .         415
Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
          420                    425                    430
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